

and allocation-driven mechanism constitutes a major bottleneck in achieving coordinated improvement of high yield and high sugar content in sugarcane breeding (Lu et al., 2024; Wu et al., 2024).

From a breeding perspective, modern sugarcane cultivars are mainly derived from interspecific hybridization between *Saccharum officinarum* and *S. spontaneum*, followed by repeated backcrossing. This system has significantly improved yield, adaptability, and stress resistance, leading to the development of many widely adopted and representative cultivars (Li et al., 2024; Wu et al., 2024). However, in recent years, genetic gains for complex traits in sugarcane breeding programs have shown signs of plateauing. This is largely due to the highly polyploid and heterozygous genome of sugarcane, long breeding cycles, complex genotype \times environment \times management interactions, and limitations in high-throughput and precise phenotyping (Lu et al., 2024). These factors constrain the effective utilization of genetic variation and have led traditional breeding to remain biased toward yield improvement rather than coordinated trait optimization. With the development of whole-genome sequencing, genome-wide association studies (GWAS), multi-population QTL mapping, and multi-omics approaches, researchers have gradually elucidated the genetic architecture of key traits such as cane yield, plant height, stalk diameter, tiller number, and sucrose content. In addition, key enzymes and regulatory networks involved in sucrose metabolism have been identified as critical factors in sugar accumulation (Li et al., 2024; Mehdi et al., 2024). Meanwhile, emerging technologies such as genomic selection, RNA interference, and gene editing provide new molecular tools to improve selection efficiency and precisely regulate carbon allocation (Brant et al., 2025; Wang et al., 2025).

This study aims to explore the theoretical basis and technical pathways for the coordinated improvement of sugarcane yield and sucrose accumulation. Although previous studies have reviewed sugarcane improvement from perspectives such as breeding history, genomics, or biorefinery applications, there is still a lack of an integrated framework that systematically links the multi-trait basis of yield and sugar accumulation, their genetic and physiological interactions, and coordinated improvement strategies under different environmental conditions. Therefore, developing a coordinated optimization framework centered on multi-trait (NTrait) integration has become a key direction for advancing efficient sugarcane breeding. This study analyzes the genetic associations and regulatory networks between yield- and sugar-related traits, summarizes advances in QTL mapping, association analysis, marker-assisted selection, and genomic selection, and further discusses multi-trait-driven breeding strategies and ideotype design. The objective is to provide a clearer theoretical foundation and methodological framework for the coordinated improvement of high yield and high sugar content, and to support the efficient utilization of sugarcane in sugar production and bioenergy systems.

2 Trait Basis of Sugarcane Yield and Sugar Content Formation

2.1 Key agronomic traits related to sugarcane yield formation

Sugarcane yield is a typical complex quantitative trait, commonly expressed as tons of cane per hectare (TCH), and primarily determined by millable cane number and single stalk weight. Traits such as plant height, stalk diameter, and internode characteristics further influence yield by affecting single stalk biomass (Tolera et al., 2024). Multi-environment trials and path analysis consistently indicate that millable cane number and single stalk weight exert the strongest direct effects on yield, making them key selection targets in breeding. Thus, yield improvement depends on the coordinated optimization of multiple component traits rather than reliance on any single trait.

At the population level, millable cane number represents the fundamental determinant of yield, integrating germination rate, emergence uniformity, tillering ability, and stalk formation efficiency. Strong early germination and tillering promote rapid canopy establishment, while a high stalk formation rate ensures effective conversion of tillers into harvestable canes, thereby stabilizing yield per unit area (Tolera et al., 2024; Vennela et al., 2024). Accordingly, genotypes combining high tillering potential with stable stalk formation capacity are more likely to achieve consistently high yields.

Single stalk traits and resource-use efficiency largely determine the upper limit of biomass accumulation. Longer and thicker stalks with well-developed internodes generally exhibit greater fresh weight and dry matter